

Genome version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 10:39:12, Search time 7:28:71 seconds
(without alignments)
28.464 Million cell updates/sec

Title: US-09-856-070-25

Perfect score: 23
Sequence: 1 MLRLQ 5

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	160	Y650_TREPA	G83656 treponema p
2	23	100.0	196	RL19_HUMAN	P14118 homo sapien
3	23	100.0	244	UL51_HSV4	G60638 equine herp
4	23	100.0	245	UL51_HSVB	P28961 equine herp
5	23	100.0	288	P8P1_SCHPO	G74456 schizosach
6	23	100.0	313	PYPR_AGR05	G8u79 agrobacteri
7	23	100.0	313	PYPR_RHIME	Q52q15 rhizobium m
8	23	100.0	317	MTB1_NEIGO	Q53603 nelisseria g
9	23	100.0	318	MTB2_HAEAE	Q30868 haemophilus
10	23	100.0	322	PYPR_BRUME	G8y662 brucella me
11	23	100.0	322	PYPR_XYLFA	G9p668 xylicella fas
12	23	100.0	323	PYPR_RALSO	G8y112 ralstonia s
13	23	100.0	326	PYPR_RHITO	Q98m86 rhizobium l
14	23	100.0	332	PYPR_CAMP	Q5a7k4 caulobacter
15	23	100.0	334	PYPR_PSEAE	Q59653 pseudomonas
16	23	100.0	334	PYPR_PSEPU	Q59711 pseudomonas
17	23	100.0	383	VJIM_ECOLI	P39184 escherichia
18	23	100.0	423	FLGH_HELMU	P58611 helicobacte
19	23	100.0	503	PUR1_PASMU	Q916b8 pasteurella
20	23	100.0	504	PUR1_HAEIN	P43854 haemophilus
21	23	100.0	580	E2R1_BCVIN	P31576 bos taurus
22	23	100.0	586	E2R1_HUMAN	F15911 homo sapien
23	23	100.0	586	PYPR_MOUSE	P26040 mus musculo
24	23	100.0	670	YQ65_CAUPI	G20466 caenorhabdi
25	21	91.3	269	N0DC_VIRCH	G9kv27 vibrio chol
26	21	91.3	289	LEF4_PSEST	G2e16 pseudomonas
27	21	91.3	366	ODR6_SCHPO	Q09171 schizosach
28	21	91.3	396	G43A_DROME	G9v629 drosophila
29	21	91.3	397	GALL_TREPA	G83433 treponema p
30	21	91.3	429	PUR2_VIRCH	G9A981 vibrio chol
31	21	91.3	437	PUR2_XYLFA	G9ec09 xylicella fas
32	21	91.3	459	YGW9_YEAST	P53083 saccharomyc
33	21	91.3	461	G6PT_PTIME	G93362 rhizobium m

RESULT 1

Y650_TREPA
ID Y650_TREPA STANDARD: PRT: 160 AA.
AC 083656;
DT 30-MAY-2000 (Ref. 39, Created)
DI 30-MAY-2000 (Ref. 39, Last sequence update)
EI 18-JUL-2001 (Ref. 40, Last annotation update)
DE Hypothetical protein TP0650.
GN TP0650.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID:160;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-Nichols;
FX MEDLINE:98442770; PubMed:9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey K.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Uitterback T.,
McDonald L., Attachi P., Bowman G., Cotton M.D., Fujii C., Garland S.,
Hatch H., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.G.,
Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis
spirochete".
RL Science 281:375-388(1998).
CC - SIMILARITY: BELONGS TO THE UPF0054 FAMILY.
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CC EMBL: AF061235, AAC55623.1;
CC TIGR: TP0650;
CC InterPro: IP0002036; UPF0054.
CC Pfam: PF02130; UPF0054; 1.
CC Prodom: P005684; UPF0054; 1.
CC TIGRfams: TIGR00043; UPF0054; 1.
CC PROSITE: PS01366; UPF0054; 1.
CC Hypothetical protein, Complete proteome.
SQ SEQUENCE 160 AA; 18612 MW; 654796A81A7L898F GRC64;

Query Match: 100.0%, Score 23; DB 1; Length 160;
Best local Similarity 100.0%; Prod. No. 13;
Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

Qv 1 MLRLQ 5

Db 137 MLRLQ 141

RESULT 2

RL19_HUMAN
AC P14118; P22908; STANDARD; PRI; 196 AA.
DT 01-JAN-1990 (Rel. 13, Created)
DI 01-JAN-1990 (Rel. 13, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L19.
GN RPL19.
OS Homo sapiens (human).
OS Mus musculus (mouse).
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE-92285147; PubMed-1598220;
RA Kumabe T., Schma Y., Yamamoto I.;
RI "Human cDNAs encoding elongation factor 1 gamma and the ribosomal
protein L19.";
RL Nucleic Acids Res. 20:2598-2598(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE-93185086; PubMed-8095182;
RA Henry J.L., Coquin D.L., King C.R.;
RI "High level expression of the ribosomal protein L19 in human breast
tumors that overexpress erbB-2.";
RL Cancer Res. 53:1403-1408(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE-91090840; PubMed-1702292;
RA Nakamura T., Ono M., Mariage-Samson P., Hillova T., Hill M.;
RI "Nucleotide sequence of mouse L19 ribosomal protein cDNA isolated in
screening with the oncogene probes.";
RL DNA Cell Biol. 9:697-703(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi F., Iyosawa H., Kondo S., Yamazaki T.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kachi P., Lewis S., Matsuo Y., Nikita T., Nishio S., Ogasawara J.,
RA Schram L.M., Staehli F., Suzuki K., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Haldarelli R., Harsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann J., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring K., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wani K.H., Weitz C., Whitaker C., Wilming L.,
RA Watanabe-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RI "Functional annotation of a full length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Strausberg R.;
RI Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC SPECIES-Rat;
RX MEDLINE-87109220; PubMed-3542997;
RA Chan Y.-L., Lin A., McNally J., Peleg D., Meyuhas O., Wool I.G.;
RI "The primary structure of rat ribosomal protein L19. A determination
from the sequence of nucleotides in a cDNA and from the sequence of
RT amino acids in the protein.";
RL J. Biol. Chem. 262:1111-1115(1987).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN-Fischer;
RX MEDLINE-95309903; PubMed-7789470;
RA Davies R., Fried M.;
RI "The L19 ribosomal protein gene (Rpl19): gene organization,
RT chromosomal mapping, and novel promoter region.";
RL Genomics 25:372-380(1995).
RN [9]
RP SIMILARITY: BELONGS TO THE L19F FAMILY OF RIBOSOMAL PROTEINS.
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CC
DR EMBL: X63527; CAA45090.1;
DR EMBL: S56985; AAB25672.1;
DR EMBL: BC000530; AAH00530.1;
DR EMBL: RC013016; AAH13016.1;
DR EMBL: M62952; AAB48630.1;
DR EMBL: AK010440; BAB26941.1;
DR EMBL: BC010710; AAH10710.1;
DR EMBL: J02650; AAA42071.1;
DR EMBL: X82302; CAA57685.1;
DR PIR: S09560; K5RT19.
DR PIR: A36554; A36554.
DR PIR: S22656; S22656.
DR PIR: A48992; A48992.
DR Genew: HGNC:10312; RPL19.
DR MIM: 180456;
DR MGI: 98020; Rpl19.
DR InterPro: IPR000196; Ribosomal_L19c.
DR Pfam: PF01280; Ribosomal_L19c; 1.
DR PROSITE: PS00526; RIBOSOMAL_L19; 1.
DR KEGG: Ribosomal protein.
FT CONFLICT 179 179 A -> S (IN REF. 4).
SQ SEQUENCE 196 AA; 23466 MW; 4AF506393F526216 CRC64;
Query Match 100.0% Score 23; DH 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
L7 1 MURIO 5
DB 3 MURIO 7
RESULT 3
U151_HSVF4
ID U151_HSVF4 STANDARD; PRT; 241 AA.
AC Q00038;
DI 01-DEC-1992 (Rel. 24, Created)
DI 01-DEC-1992 (Rel. 24, Last sequence update)
DI 01-DEC-1992 (Rel. 24, Last annotation update)
DE Gene 8 protein.
GN 8 OR B2
OS Equine herpesvirus type 4 (strain 1942) (EHV 4) (equine herpesvirus
OS type 1 subtype 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10333;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE-91202570; PubMed=1850013;
RA Whittaker G.R., Riggio M.P., Halliburton I.W., Killington R.A.,
RI Allen G.P., Meredith D.M.;
RT "Antigenic and protein sequence homology between gp13/14, a herpes
RT simplex virus type 1 tegument protein, and gp10, a glycoprotein of
PL equine herpesvirus 1 and 4.";
PL J. Virol. 65:2420-2426(1991);
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 US15.
CC EHV-1 8, AND VZV 7.
CC
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CC
CC EMBL: X17684; CAA35668.1;
DR PIR: S36703; S36703;
SQ SEQUENCE 244 AA; 35209AA; 430999; 68931;
Query Match 100.0%; Score 23, DB 1, Length 244,
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
OY 1 MLRQ 5
DB 34 MLRQ 38
IIII
RESULT 4
U151_HSVB STANDARD; PRT; 245 AA.
AC P28961;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DI 01-DEC-1992 (Rel. 24, Last annotation update)
DE Gene 8 protein.
GN 8.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1)
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus
OX NCBI_taxid=31520;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92295566; PubMed=1318606;
RA Telford E.A.R., Watson M.S., McBride K., Davidson A.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992);
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 US15.
CC EHV-1 8, AND VZV 7.
CC
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CC
CC EMBL: M86664; AAR02443.1;
DR PIR: I36795; W/HER7. 26365 MW; 265804AAR0242A5; Q8764.
SQ SEQUENCE 245 AA; 26365 MW; 265804AAR0242A5; Q8764.
Query Match 100.0%; Score 23, DB 1, Length 245,
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
OY 1 MLRQ 5
DB 33 MLRQ 37
IIII

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RESULT 5
PEFL_SCHPO STANDARD; PRT; 288 AA.
AC 074456;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sorine/threonine-protein kinase pefl (EC 2.7.1.37) (Cyclin-dependent
DE kinase pefl) (PHO85 homolog).
GN PEFL; AK: SP031604.11.
OS Schizosaccharomyces pombe (fission yeast).
CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
CC Schizosaccharomycetes.
CX NCBI_taxid=4890;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN 972;
RX MEDLINE-20437747; PubMed=10982385;
RA Tanaka K., Okajima H.;
RT "A pol-like cyclin activates the Koz2p-Cdc10p cell cycle 'start'
RT transcriptional factor complex in fission yeast.";
PL Mol. Biol. Cell 11:2845-2862(2000);
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-972;
RX MEDLINE-21848401; PubMed=11859360;
RA Wood V., Gwilliam P., Palandream M.A., Lyne M., Lyne P., Stewart A.,
RA Squires J., Pear N., Hayles T., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald D., McLean J.,
RA Mocher P., Mouton S., Muddell K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Sanger K., Sharp S.,
RA Skelton J., Simmonds M., Squires P., Squires S., Stevens K.,
RA Taylor K., Taylor R.G., Tacey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert P., P-then T., Grygorczyk B.,
RA Woldjens I., Vanstreels E., Rieder M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Frilze G., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Heck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Mottier S.,
RA Galibert F., Aves S., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Kuchel M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga P.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Camigeros A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Corradi F., Lowe T., McCombie W.P., Paulsen O., Petashkin J.,
RA Sipakowski G.V., Ussery D., Harrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
PL Nature 415:871-882(2002).
CC -!- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with the pefl cyclin.
CC -!- SIMILARITY: BELONGS TO THE SHK/INK FAMILY OF PROTEIN KINASES.
CC CDC2/COKX SUBFAMILY.
CC
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CC
CC EMBL: A031535; CAA02750.1;
DR EMBL: A045127; BAB16402.1;
DR HSP; P24941; 1CKP.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
|||||

DT 222 MLRQ 226

RESULT 8

MTBL NEIGO STANDARD; PRT; 317 AA.

AC Q59603:

DI 16-OCT-2001 (Rel. 40, Last sequence update)

DI 16-OCT-2001 (Rel. 40, Last sequence update)

DE Modification methylease NqoI (EC 2.1.1.73) (Cytosine specific

DE methyltransferase NqoBI (M.NqoBI) (M.NqoI).

GN NqoBIM.

OS Neisseria gonorrhoeae

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN: WP392;

RX MEDLINE: 98290322; PubMed: 9628358;

RA Stein D.C., Gunn J.S., Plekharowicz A.

RT "Sequence similarities between the genes encoding the S.NqoI and HaeII restriction/modification systems."

RL Biol. Chem. 379:575-578(1998).

CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE

CC KGGGCG. CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRAINS, AND

CC PROTECTS THE DNA FROM CLEAVAGE BY THE HAEII ENDONUCLEASE.

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-

CC adenosyl-L-homocysteine + DNA 5-methylcytosine.

CC -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY

CC

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CC

CC PDB: 1U2459; AAR03206 2;

DR HSSP: P05102; GMIT.

DR REBASE: 3607; M.NqoBI.

DR InterPro: IPR001525; C5_DNA_meth

DR Pfam: PF00145; DNA_methylase; 1.

DR PRINTS: PR00105; C5METHYTRFAS

DR TIGRFAMS: TIGR00675; dcm; 1.

DR PROSITE: PS00094; C5_MTASE_1; 1.

DR PROSITE: PS00095; C5_MTASE_2; FALSE_NEG.

KW Transferase; Methyltransferase; Restriction system.

FT ACT_SITE 71 71 BY SIMILARITY.

SQ SEQUENCE 317 AA; 35949 MW; F0549A5259A141 CQC64;

Query Match 100.0%; Score 23; DB 1; Length 317.

Best Local Similarity 100.0%; Pred. No. 28;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 MLRQ 5
|||||

DT 256 MLRQ 256

RESULT 9

MTBL HAEII STANDARD; PRT; 318 AA.

AC Q30868:

DI 16-OCT-2001 (Rel. 40, Created)

DI 16-OCT-2001 (Rel. 40, Last sequence update)

DE Modification methylease HaeII (EC 2.1.1.73) (Cytosine specific

DE methyltransferase HaeII (M.HaeII) (M.HaeI).

GN HaeIIM.

OS Haemophilus aegyptius

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

OX NCBI_TaxID=725;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN: ATCC 11116;

RX MEDLINE: 98290322; PubMed: 9628358;

RA Stein D.C., Gunn J.S., Plekharowicz A.

RT "Sequence similarities between the genes encoding the S.NqoI and HaeII restriction/modification systems."

RL Biol. Chem. 379:575-578(1998).

CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE

CC KGGGCG. CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRAINS, AND

CC PROTECTS THE DNA FROM CLEAVAGE BY THE HAEII ENDONUCLEASE.

CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-

CC adenosyl-L-homocysteine + DNA 5-methylcytosine.

CC -1- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.

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CC

CC PDB: 1U2459; AAR03206 2;

DR HSSP: P05102; GMIT.

DR REBASE: 3607; M.NqoBI.

DR InterPro: IPR001525; C5_DNA_meth

DR Pfam: PF00145; DNA_methylase; 1.

DR PRINTS: PR00105; C5METHYTRFAS

DR TIGRFAMS: TIGR00675; dcm; 1.

DR PROSITE: PS00094; C5_MTASE_1; 1.

DR PROSITE: PS00095; C5_MTASE_2; FALSE_NEG.

KW Transferase; Methyltransferase; Restriction system.

FT ACT_SITE 71 71 BY SIMILARITY.

SQ SEQUENCE 317 AA; 35949 MW; F0549A5259A141 CQC64;

Query Match 100.0%; Score 23; DB 1; Length 317.

Best Local Similarity 100.0%; Pred. No. 28;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 MLRQ 5
|||||

DT 256 MLRQ 256

RESULT 10

PYRB BRUME STANDARD; PRT; 322 AA.

AC Q8YC62:

DI 15-JUN-2002 (Rel. 41, Created)

DI 15-JUN-2002 (Rel. 41, Last sequence update)

DI 15-JUN-2002 (Rel. 41, Last annotation update)

DE Aspartate carboxymethyltransferase (EC 2.1.3.2) (Aspartate

DE transcarbamylase) (AUCCase).

GN PYRB OR HME110670.

OS Brucella melitensis.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OX NCBI_TaxID=29459;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN: 16M / ATCC 23456 / Biotype 1;

RX MEDLINE: 20020109; PubMed: 11756688;

RA DelVecchio V.G., Kapural V., Redkar R.J., Patra G., Muir G., Los T.,

RA Ikavara N., Anderson L., Bhattacharya A., Lkakis A., Peckif G.,

PA Ishewski J., Larson N., O'Souza M., Petral A., Marat M., Sultman E.,

PA Solikow E., Elzer R.H., Hagius S., O'Callaghan D., Letesson J.J.,

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RA Basilekova R., Kyriakides N., Overbeck R.,
RT "The genome sequence of the facultative intracellular pathogen
RA Brucella melitensis".
RA Proc. Natl. Acad. Sci. U.S.A. 99:447-448(2002)
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
CC + N-carbamoyl-L-aspartate.
CC -!- PATHWAY: Pyrimidine biosynthesis; second step.
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC
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CC
DR EMBL: A009702; AAL5912.1; -.
DR InterPro: IPR002029; Asp/orn_Corranf
DR InterPro: IPR002082; Asp_carmbitransf.
DR Pfam: PF00185; OTCace_1.
DR Pfam: PF02729; OTCace_N_1.
DR PRINTS: PR00100; AOTCASE
DR TIGRFAMs: TIGR00670; asp_carb1tr; 1.
DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
KW Pyrimidine biosynthesis, Transferase, Complete proteome.
SQ SEQUENCE 322 AA; 34892 MW; 8136298851B4521B CRC64.

Query Match 100.0%; Score 23; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLQ 5
DB 228 MRLQ 232
|||||

RESULT 11
PYRR_XYLEA
ID PYRR_XYLEA STANTAPD: PPT: 322 AA.
QYPR68:
DI 15 JUN-2002 (Rel. 41, Created)
DI 15 JUN-2002 (Rel. 41, Last sequence update)
DI 15 JUN-2002 (Rel. 41, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
DE Transcarbamylase) (ATCase).
GN PYRR OR XF2226.
OR Xylella fastidiosa.
OR Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OR Xylella.
OX NCBI_TaxID=2371;
|||
SEQUENCE FROM N.A.
MEDLINE:20465717; PubMed:10910447;
STRAIN:9456;
RA Simpson A.J.G., Reichach F.C., Arruda P., Abreu F.A., Aceneto M.,
RA Alvares R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Fordin S., Bove J.M., Briones M.E.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.H., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorty H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Frana J.S., Franca S.G., Franco M.G., Frohme M., Furlan L.R.,
RA Gardner J.S., Goldman G.H., Goldman M.H.S., Gomes S.T., Gruber A.,
RA Ho P.L., Holsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramao E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.J., Nobrega F.C., Nunes L.P., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

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RA Peixoto R.R., Pereira G.A.G., Pereira H.A. Jr., Pasquero J.H.,
RA Quaggio R.B., Roberto P.C., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.F., da Silva A.M., da Silva F.E., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siquela W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Isubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa".
RL Nature 406:151-159(2000).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
CC + N-carbamoyl-L-aspartate.
CC -!- PATHWAY: Pyrimidine biosynthesis; second step.
CC -!- SUBUNIT: CONTAINS SIX CATALYTIC AND SIX REGULATORY CHAINS (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
CC
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CC
DR EMBL: A004045; AAF85025.1; -.
DR DDB: D00479; 3CSD.
DR InterPro: IPR002029; Asp/orn_Corranf.
DR InterPro: IPR002082; Asp_carmbitransf.
DR TIGRFAMs: TIGR00185; OTCace_1.
DR Pfam: PF00185; OTCace_1.
DR Pfam: PF02729; OTCace_N_1.
DR PRINTS: PR00100; AOTCASE.
DR TIGRFAMs: TIGR00670; asp_carb1tr; 1.
DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
KW Pyrimidine biosynthesis, Transferase, Complete proteome.
SQ SEQUENCE 322 AA; 34637 MW; 01D05C04F5A7EAD CRC64.

Query Match 100.0%; Score 23; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLQ 5
DB 237 MRLQ 241
|||||

RESULT 12
PYRR_RALSO
ID PYRR_RALSO STANDARD: PPT: 323 AA.
AC Q8Y112;
DI 15 JUN-2002 (Rel. 41, Created)
DI 15 JUN-2002 (Rel. 41, Last sequence update)
DI 15 JUN-2002 (Rel. 41, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
DE Transcarbamylase) (ATCase).
GN PYRR OR RSC0678 OR RSC0583.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria, beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
|||
SEQUENCE FROM N.A.
STRAIN:GM11000;
EX MEDLINE:21681879; PubMed:11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Manqnot S.,
RA Arlet M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Chelcoun N., Claudel-Reward C., Cunne S., Demange N.,
RA Caspin C., Lavoie M., Moisan A., Robert C., Saurin W., Schick T.,
RA Siquier P., Thebaud P., Whalen M., Winkler P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum".
RL Nature 415:497-502(2002).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate

```

CC N-carbamoyl-L-aspartate.
 CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -1- SIMILARITY: BELONGS TO THE AICASES/OTCASES FAMILY.
 CC
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 CC
 DR EMBL: AL646060; CAU14208.1; -
 DR InterPro: IPR002029; Asp_gln_cotranf.
 DR InterPro: IPR002082; Asp_carbmitransf.
 DR Pfam: PF00185; OTCase_N; 1
 DR Pfam: PF02729; OTCase_N; 1
 DR PRINTS: PR00100; AOTCASE.
 DR TIGRfams: TIGR00670; asp_carb_tr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERSH; 1.
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 323 AA; 35133 MW; 1706DA04403E20T2 CR664;

 Query Match 100.0%; Score 23; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLRLQ 5
 DB 237 MLRLQ 241

 RESULT 13
 PYR_RHILQ
 ID PYR_RHILQ STANDARD: PPT: 326 AA.
 AC Q98M86;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
 DE transcarbamylase) (ATCase).
 GN PYR OR MR0686.
 OS Rhizobium loti (Mesorhizobium loti)
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T, Nakamura Y, Sato S, Asamizu E, Yano T, Sasamoto S,
 RA Watanabe A, Idesawa K, Ishikawa A, Kawashima K, Kimura T,
 RA Kishida Y, Kiyokawa C, Kohara M, Matsushima M, Matsuno A,
 RA Mochizuki Y, Nakayama S, Nakazaki N, Shimo S, Sugimoto M,
 RA Takeuchi C, Yamada M, Takata S;
 RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RA Mesorhizobium loti".
 RL DNA Res. 7:331-338(2000).
 CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate -> phosphate
 CC + N-carbamoyl-L-aspartate.
 CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -1- SIMILARITY: BELONGS TO THE AICASES/OTCASES FAMILY.
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 CC
 DR EMBL: AP002995; BAB16227.1; -
 DR InterPro: IPR002029; Asp_gln_cotranf

DR InterPro: IPR002082; Asp_carbmitransf.
 DR Pfam: PF00185; OTCase_N; 1.
 DR Pfam: PF02729; OTCase_N; 1.
 DR PRINTS: PR00100; AOTCASE.
 DR TIGRfams: TIGR00670; asp_carb_tr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERSH; 1.
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 326 AA; 35212 MW; E75A614059F3D5 CR664;

 Query Match 100.0%; Score 23; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLRLQ 5
 DB 228 MLRLQ 232

 RESULT 14
 PYR_CAUCR
 ID PYR_CAUCR STANDARD: PPT: 332 AA.
 AC Q9A5K4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
 DE transcarbamylase) (ATCase).
 GN PYR OR G2443.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AICC 14089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen O., Nelson K.E.,
 RA Eisen J., Heidelberg J.P., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely R.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Graven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Krumholz M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro B., Fraser C.M.;
 RA "Complete genome sequence of Caulobacter crescentus".
 RL EMBL: X61111; S1 - S A 34 436 434(591).
 CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate -> phosphate
 CC + N-carbamoyl-L-aspartate.
 CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -1- SIMILARITY: BELONGS TO THE AICASES/OTCASES FAMILY.
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 CC
 DR EMBL: AE005913; AAK24414.1; -
 DR HSSP: P00479; ACSU.
 DR TIGRfams: TIGR00670; asp_carb_tr; 1.
 DR InterPro: IPR002029; Asp_gln_cotranf.
 DR InterPro: IPR002082; Asp_carbmitransf.
 DR Pfam: PF00185; OTCase_N; 1.
 DR Pfam: PF02729; OTCase_N; 1.
 DR PRINTS: PR00100; AOTCASE.
 DR TIGRfams: TIGR00670; asp_carb_tr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERSH; 1.
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 332 AA; 35509 MW; 13261C5C131AE4 CR664;

 Query Match 100.0%; Score 23; DB 1; Length 332;
 Best Local Similarity 100.0%; Pred. No. 29;

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Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1 MLRLQ 5
      |||||
DB      241 MLRLQ 245

Search completed: January 16, 2003, 16:51:16
Job time . 9.28571 secs

RESULTS 15
PYRB_PSEAF
ID PYRB_PSEAF STANDARD; PRT: 334 AA.
AC Q59653;
DE 01-NOV-1997 (Rel. 35, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
DE L-asparbamylase) (AICase).
GN PYRB OR PA0402.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
CX NCBI_TaxID=287;
LN [1]
RP SEQUENCE FROM N.A.
RA STRAIN ATCC 15692 / PA01;
RA Virekrey J.F., Schurr M.J., Benjamin R.C., Clinin R., Shantley M.S.,
RA O'Donovan G.A.;
RA Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
LN [2]
RP SEQUENCE FROM N.A.
RA STRAIN ATCC 15692 / PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Blekey M.J., Brinkman F.S.L., Hutnagle W.G., Kowalik D.J., Lagrou M.,
RA Garber R.L., Gentry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.A., Coulter S.N., Folger K.P., Kas A., Jarbq K., Lim P.M.,
RA Smith K.A., Spencer D.H., Wong C.K.-S., Wu Z., Paulsen I.T.,
RA Keizer J., Sator M.H., Hancock R.R.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RA opportunistic pathogen."
RA Nature 406:959-964 (2000).
CC -1 CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
CC + N-carbamoyl-L-aspartate.
CC -1 PATHWAY: pyrimidine biosynthesis; second step.
CC -1 SUBUNIT: HETERODIMER OF 6 ACTIVE PYRB SUBUNITS AND 6 NON-
CC CATALYTIC PYRB SUBUNITS (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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DR EMBL: L19649; AAAJ5976.1; -
DR EMBL: AE004477; AAG03791.1; -
DR USSP: P00479; 3CS0.
DR InterPro: IPR002029; Asp/orn_CoTransf.
DR InterPro: IPR002082; Asp_carbamyltransf.
DR Pfam: PF00185; OTCace; 1.
DR Pfam: PF02729; OTCace_N; 1.
DR PRINTS: PK00100; AOTCASE.
DR TIGRfam: TIGR00670; asp_carb_tr; 1.
DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
KW Pyrimidine biosynthesis; Transferase; Complete proteome.
FT CONFLICT 206 206 R -> A (IN REF. 1).
SQ SEQUENCE 334 AA; 36629 MW; 2DC90450FA2442E9 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 334;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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